

SEQUENCE LISTING

<110> MARINE BIOTECHNOLOGY INSTITUTE CO., LTD.

<120> METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS USING GYRASE GENE AS
AN INDICATOR

<130> PH-581

<140> US09/208, 688

<141> 1998-12-10

<150> JP97/343316

<151> 1997-12-12

<160> 80

<170> PatentIn version 2.0

<210> 1

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<212> DNA

<213> Bacteroides vulgatus

<220>

<221> CDS

<222> (1)... (1212)

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165	170	175		
ata gaa ggc ggt aca cac gag gcc ggt ttc cgc agc gca tta acc cgt	576			
Ile Glu Gly Gly Thr His Glu Ala Gly Phe Arg Ser Ala Leu Thr Arg				
180	185	190		
gta ctg aag aaa tat gcg gaa gat acc aaa gca ctg gaa aaa gca aaa	624			
Val Leu Lys Lys Tyr Ala Glu Asp Thr Lys Ala Leu Glu Lys Ala Lys				
195	200	205		
gtc gag att tcg gga gag gac ttc cgc gaa ggc ttg att gcc gtc att	672			
Val Glu Ile Ser Gly Glu Asp Phe Arg Glu Gly Leu Ile Ala Val Ile				
210	215	220		
tca gtg aaa gta gcc gag ccg cag ttc gaa gga cag acc aag acc aag	720			
Ser Val Lys Val Ala Glu Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys				
225	230	235	240	
ctg ggc aac agc gaa gtg agt ggt gcc gtg aac caa gct gta ggc gaa	768			
Leu Gly Asn Ser Glu Val Ser Gly Ala Val Asn Gln Ala Val Gly Glu				
245	250	255		
gcg ctt aca tat tat ctg gaa gaa cat ccg aaa gaa gca aaa cag att	816			
Ala Leu Thr Tyr Tyr Leu Glu Glu His Pro Lys Glu Ala Lys Gln Ile				
260	265	270		
gtt gac aaa gtg atc ctg gct gca aca gcg cgt atc gcc gca cgc aag	864			
Val Asp Lys Val Ile Leu Ala Ala Thr Ala Arg Ile Ala Ala Arg Lys				
275	280	285		
gca cgt gaa tct gtt caa aga aag agt ccg atg ggc ggt ggc gga ctg	912			
Ala Arg Glu Ser Val Gln Arg Lys Ser Pro Met Gly Gly Gly Gly Leu				
290	295	300		
ccg ggc aaa ctg gcc gac tgc tcg agc cgt aat ccg gag gaa tgt gaa	960			

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Gly	Gly	Lys	Ile	Tyr	Gln	Gln	Glu	Tyr	Ser	Cys	Gly	His	Pro	Leu	Tyr				
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Ser	Val	Lys	Glu	Val	Gly	Thr	Ala	Asp	Ile	Thr	Gly	Thr	Lys	Gln	Thr				
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Phe	Trp	Pro	Asp	Asp	Thr	Ile	Phe	Thr	Val	Thr	Glu	Tyr	Lys	Phe	Asp				
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Ile	Leu	Gln	Ala	Arg	Met	Arg	Glu	Leu	Ala	Tyr	Leu	Asn	Lys	Gly	Ile				
85					90					95									
Thr	Ile	Ser	Leu	Thr	Asp	Arg	Arg	Ile	Lys	Glu	Glu	Asp	Gly	Ser	Phe				
100					105					110									
Lys	Lys	Glu	Ile	Phe	His	Ser	Asp	Glu	Gly	Val	Lys	Glu	Phe	Val	Arg				
115					120					125									
Phe	Leu	Asn	Arg	Asn	Asn	Glu	Ala	Leu	Ile	Asn	Asp	Val	Ile	Tyr	Leu				
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Asn	Thr	Glu	Lys	Asn	Asn	Thr	Pro	Ile	Glu	Cys	Ala	Ile	Met	Tyr	Asn				
145					150					155					160				
Thr	Gly	Tyr	Arg	Glu	Ser	Leu	His	Ser	Tyr	Val	Asn	Asn	Ile	Asn	Thr				
165					170					175									
Ile	Glu	Gly	Gly	Thr	His	Glu	Ala	Gly	Phe	Arg	Ser	Ala	Leu	Thr	Arg				
180					185					190									
Val	Leu	Lys	Lys	Tyr	Ala	Glu	Asp	Thr	Lys	Ala	Leu	Glu	Lys	Ala	Lys				
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Val	Glu	Ile	Ser	Gly	Glu	Asp	Phe	Arg	Glu	Gly	Leu	Ile	Ala	Val	Ile				
210					215					220									
Ser	Val	Lys	Val	Ala	Glu	Pro	Gln	Phe	Glu	Gly	Gln	Thr	Lys	Thr	Lys				
225					230					235					240				
Leu	Gly	Asn	Ser	Glu	Val	Ser	Gly	Ala	Val	Asn	Gln	Ala	Val	Gly	Glu				
245					250					255									

Variable	Mean	SD	Min	Max
Age	38.5	10.2	22	55
Gender	Male	Female		
Marital Status	Married	Single		
Education	High School	College		
Occupation	Manager	Worker		
Income	\$30,000	\$40,000		
Health Status	Good	Fair		
Stress Level	Low	High		
Life Satisfaction	High	Low		
Work-Life Balance	Good	Poor		
Family Support	Strong	Weak		
Community Involvement	Active	Passive		
Religious Beliefs	Religious	Secular		
Political Views	Conservative	Liberal		
Environmental Concern	High	Low		
Technology Use	Frequent	Infrequent		
Travel Habits	Frequent	Infrequent		
Dietary Preferences	Vegetarian	Non-Vegetarian		
Exercise Routine	Regular	Irregular		
Sleep Patterns	Regular	Irregular		
Substance Use	None	Occasional		
Personal Goals	Clear	Vague		
Resilience	High	Low		
Empathy	High	Low		
Communication Skills	Good	Poor		
Conflict Resolution	Effective	Ineffective		
Decision Making	Rational	Emotional		
Time Management	Good	Poor		
Organization	High	Low		
Attention Span	Long	Short		
Memory	Good	Poor		
Learning Style	Visual	Auditory		
Problem Solving	Creative	Conventional		
Adaptability	High	Low		
Flexibility	High	Low		
Openness	High	Low		
Conscientiousness	High	Low		
Agreeableness	High	Low		
Neuroticism	Low	High		
Extraversion	High	Low		
Introversion	Low	High		
Social Skills	Good	Poor		
Interpersonal Relationships	Healthy	Unhealthy		
Self-Confidence	High	Low		
Self-Esteem	High	Low		
Self-Motivation	High	Low		
Goal Setting	Clear	Vague		
Time Management	Good	Poor		
Organization	High	Low		
Attention Span	Long	Short		
Memory	Good	Poor		
Learning Style	Visual	Auditory		
Problem Solving	Creative	Conventional		
Adaptability	High	Low		
Flexibility	High	Low		
Openness	High	Low		
Conscientiousness	High	Low		
Agreeableness	High	Low		
Neuroticism	Low	High		
Extraversion	High	Low		
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Social Skills	Good	Poor		
Interpersonal Relationships	Healthy	Unhealthy		
Self-Confidence	High	Low		
Self-Esteem	High	Low		
Self-Motivation	High	Low		
Goal Setting	Clear	Vague		
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Attention Span	Long	Short		
Memory	Good	Poor		
Learning Style	Visual	Auditory		
Problem Solving	Creative	Conventional		
Adaptability	High	Low		
Flexibility	High	Low		
Openness	High	Low		
Conscientiousness	High	Low		
Agreeableness	High	Low		
Neuroticism	Low	High		
Extraversion	High	Low		
Introversion	Low	High		
Social Skills	Good	Poor		
Interpersonal Relationships	Healthy	Unhealthy		
Self-Confidence	High	Low		
Self-Esteem	High	Low		
Self-Motivation	High	Low		
Goal Setting	Clear	Vague		
Time Management	Good	Poor		
Organization	High	Low		
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Memory	Good	Poor		
Learning Style	Visual	Auditory		
Problem Solving	Creative	Conventional		
Adaptability	High	Low		
Flexibility	High	Low		
Openness	High	Low		
Conscientiousness	High	Low		
Agreeableness	High	Low		
Neuroticism	Low	High		
Extraversion	High	Low		
Introversion	Low	High		

7

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35 40 45
Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
50 55 60
Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu
65 70 75 80
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
85 90 95
Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp
100 105 110
Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Gln
115 120 125
Ala Ala Glu Ser Ala Lys Pro His Lys Val Lys His Arg Thr Phe His
130 135 140
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
145 150 155 160
Asn Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly
165 170 175
His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
180 185 190
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
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<212> DNA

<213> *Flavobacterium aquatile*

<220>

<221> CDS

<222> (1)... (537)

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Ser Cys Val Asn Ala Leu Ser Asp Asn Leu Lys Ala Thr Val Phe Arg
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gac gga aaa gtg tac gag caa gaa tat gaa aaa ggt aaa gca atg tat 144
Asp Gly Lys Val Tyr Glu Gln Glu Tyr Glu Lys Gly Lys Ala Met Tyr
35 40 45
ccg gtt aag caa gtt ggt gaa aca aca aag cga gga aca atg gtt act 192
Pro Val Lys Gln Val Gly Glu Thr Thr Lys Arg Gly Thr Met Val Thr
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ttt cat cct gat aaa acc att ttt act caa aca att gag tat tct tat 240
Phe His Pro Asp Lys Thr Ile Phe Thr Gln Thr Ile Glu Tyr Ser Tyr
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gat aca ctt gca gca cgt atg cgt gaa tta tct ttc ctg aat aaa gga 288
Asp Thr Leu Ala Ala Arg Met Arg Glu Leu Ser Phe Leu Asn Lys Gly
85 90 95
att aca atc aca ctt aca gat aaa aga cat act aaa gac aac ggc gat 336

ggc	gag	aac	agc	ggc	tac	acc	gtc	agc	ggg	ggg	tig	cac	gga	gtg	ggc	48
Gly	Glu	Asn	Ser	Gly	Tyr	Thr	Val	Ser	Gly	Gly	Leu	His	Gly	Val	Gly	
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gtg	tcg	gtg	gtc	aac	gcg	ctg	tcc	acc	cgc	ctg	gag	gtc	acc	atc	aag	96
Val	Ser	Val	Val	Asn	Ala	Leu	Ser	Thr	Arg	Leu	Glu	Val	Thr	Ile	Lys	
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cgc	gac	ggg	cac	gag	tgg	ttt	cag	tac	tac	gac	cgc	gcc	gtg	ccc	gga	144
Arg	Asp	Gly	His	Glu	Trp	Phe	Gln	Tyr	Tyr	Asp	Arg	Ala	Val	Pro	Gly	
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acc	ctc	aag	cag	ggc	gag	gcc	acc	aag	aag	acc	gga	acc	acg	atc	agg	192
Thr	Leu	Lys	Gln	Gly	Glu	Ala	Thr	Lys	Lys	Thr	Gly	Thr	Thr	Ile	Arg	
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ttc	tgg	gcg	gac	ccc	gaa	atc	ttc	gaa	acc	aca	cag	tac	gac	ttc	gag	240
Phe	Trp	Ala	Asp	Pro	Glu	Ile	Phe	Glu	Thr	Thr	Gln	Tyr	Asp	Phe	Glu	
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acc	gtg	gcg	cgg	cgg	ctg	cag	gag	atg	gcc	ttc	ctc	aac	aag	ggc	ctc	288
Thr	Val	Ala	Arg	Arg	Leu	Gln	Glu	Met	Ala	Phe	Leu	Asn	Lys	Gly	Leu	
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acc	atc	aac	ctc	acc	gac	gaa	cga	gtg	gag	cag	gac	gag	gtc	gtc	gac	336
Thr	Ile	Asn	Leu	Thr	Asp	Glu	Arg	Val	Glu	Gln	Asp	Glu	Val	Val	Asp	
					100					105					110	
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Glu	Val	Val	Ser	Asp	Thr	Ala	Glu	Ala	Pro	Lys	Ser	Ala	Glu	Glu	Lys	
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Ala	Ala	Glu	Ser	Thr	Ala	Pro	His	Lys	Val	Lys	His	Arg	Thr	Phe	His	
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agc ccg atc cag cag agc gtc atc gat ttc gac ggc aag ggc acc ggc				528
Ser Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly				
165	170	175		
cac gag gtc gag atc gcc atg cag tgg aac ggc ggc tac tcg gag tcc				576
His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser				
180	185	190		
gtc cac acc ttc gcc aac acc atc aac acg cac gag ggc ggc acc cac				624
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His				
195	200	205		
gag gag ggc ttc cgc agc gcg ctg acg tcg gtg gtg aac aag tac gcc				672
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala				
210	215	220		
aaa gac aag aaa ctg ctg aag gac aaa gat ccc aac ctc acc ggt gac				720
Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp				
225	230	235	240	
gac atc cgt gag ggc ttg gcc gcg gtc atc tcg gtg aag gtc gcc gag				768
Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu				
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<212> PRT

<213> *Mycobacterium asiaticum*

<400> 10

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 ggc gaa acg ttg acg gaa tat ctg gaa ttc cat ccc agc gtt gcc gat 1008
 Gly Glu Thr Leu Thr Glu Tyr Leu Glu Phe His Pro Ser Val Ala Asp
 325 330 335
 ttg atc ctc gaa aaa gcg att caa gcc ttt aat gcg gct gag gca gcg 1056
 Leu Ile Leu Glu Lys Ala Ile Gln Ala Phe Asn Ala Ala Glu Ala Ala
 340 345 350
 cga cgg gca cgg gaa ttg gtg cgt cgc aaa tca gtg ctg gaa tct tcg 1104
 Arg Arg Ala Arg Glu Leu Val Arg Arg Lys Ser Val Leu Glu Ser Ser
 355 360 365
 aca ttg ccc ggt aaa tta gca gac tgt tcc agt cgc gat ccc ggt gaa 1152
 Thr Leu Pro Gly Lys Leu Ala Asp Cys Ser Ser Arg Asp Pro Gly Glu
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<210> 14

<211> 390

<212> PRT

<213> Synechococcus sp.

<400> 14

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130 135 140	
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Trp Asn Asp Ser Phe Asn Glu Asn Leu Leu Cys Phe Thr Asn Asn Ile	
145 150 155 160	
ccg cag cgc gat ggc ggt act cac ctg gtg ggt ttc cgt tcc gcc ctg	528
Pro Gln Arg Asp Gly Gly Thr His Leu Val Gly Phe Arg Ser Ala Leu	
165 170 175	
acg cgt aac ctc aat acg tat atc gaa gcc gaa ggc ctg gcg aag aag	576
Thr Arg Asn Leu Asn Thr Tyr Ile Glu Ala Glu Gly Leu Ala Lys Lys	
180 185 190	
cac aag gtc gcg acc acc ggt gac gat gcc cgt gaa ggc ctg gcc gcg	624
His Lys Val Ala Thr Thr Gly Asp Asp Ala Arg Glu Gly Leu Ala Ala	
195 200 205	
atc att tcg gta aaa gtg ccg gat ccg aag ttc agc tcc cag acc aag	672
Ile Ile Ser Val Lys Val Pro Asp Pro Lys Phe Ser Ser Gln Thr Lys	
210 215 220	
gac aag ctg gtt tct tcc gaa gtg aag acc gcg gtc gaa cag gaa atg	720
Asp Lys Leu Val Ser Ser Glu Val Lys Thr Ala Val Glu Gln Glu Met	
225 230 235 240	
ggc aag tac ttc tcc gac ttc ctg ctg gaa aac ccg aac gaa gcc aag	768
Gly Lys Tyr Phe Ser Asp Phe Leu Leu Glu Asn Pro Asn Glu Ala Lys	
245 250 255	
ctg gtt gtc ggc aag atg atc gac gcg gca cgt gct cgt gaa gcg gcg	816
Leu Val Val Gly Lys Met Ile Asp Ala Ala Arg Ala Arg Glu Ala Ala	
260 265 270	
cgc aag acc cgt gag atg acc cgc cgc aaa ggc gcg ctg gac atc gcc	864
Arg Lys Thr Arg Glu Met Thr Arg Arg Lys Gly Ala Leu Asp Ile Ala	

Trp Asn Asp Ser Phe Asn Glu Asn Leu Leu Cys Phe Thr Asn Asn Ile
 145 150 155 160
 Pro Gln Arg Asp Gly Gly Thr His Leu Val Gly Phe Arg Ser Ala Leu
 165 170 175
 Thr Arg Asn Leu Asn Thr Tyr Ile Glu Ala Glu Gly Leu Ala Lys Lys
 180 185 190
 His Lys Val Ala Thr Thr Gly Asp Asp Ala Arg Glu Gly Leu Ala Ala
 195 200 205
 Ile Ile Ser Val Lys Val Pro Asp Pro Lys Phe Ser Ser Gln Thr Lys
 210 215 220
 Asp Lys Leu Val Ser Ser Glu Val Lys Thr Ala Val Glu Gln Glu Met
 225 230 235 240
 Gly Lys Tyr Phe Ser Asp Phe Leu Leu Glu Asn Pro Asn Glu Ala Lys
 245 250 255
 Leu Val Val Gly Lys Met Ile Asp Ala Ala Arg Ala Arg Glu Ala Ala
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tta gca gac tgt tcc agt cgc gat ccc ggt gaa tct gaa atc ttc atc	96
Leu Ala Asp Cys Ser Ser Arg Asp Pro Gly Glu Ser Glu Ile Phe Ile	
20 25 30	
gtg gaa ggg gat tgc gca ggt ggc agt gct aaa cag ggg cgc gat cgc	144
Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Gly Arg Asp Arg	
35 40 45	
cgc ttc caa gcc atc ctg cct ctg cgc ggc aaa atc ctc aac atc gag	192
Arg Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Ile Glu	
50 55 60	
aaa acg gac gat gcc aaa atc tac aaa aac act gag atc caa gcc ctg	240
Lys Thr Asp Asp Ala Lys Ile Tyr Lys Asn Thr Glu Ile Gln Ala Leu	
65 70 75 80	
att aca gcg ctg ggc ctc gga att aaa ggg gag gaa ttt gat gct tcc	288
Ile Thr Ala Leu Gly Leu Gly Ile Lys Gly Glu Glu Phe Asp Ala Ser	
85 90 95	
caa ctg cgc tac cac cgt att gtg atc atg act gac gcg gac gtc gat	336
Gln Leu Arg Tyr His Arg Ile Val Ile Met Thr Asp Ala Asp Val Asp	
100 105 110	
ggt gcg cac atc cgt acc ctc ttg ctc acc ttc ttc tat cgc tat cag	384
Gly Ala His Ile Arg Thr Leu Leu Leu Thr Phe Phe Tyr Arg Tyr Gln	
115 120 125	
cga tgc ctg ctg gag cag ggc tac atg tac att gcc tgc ccg ccg ctg	432
Arg Ser Leu Leu Glu Gln Gly Tyr Met Tyr Ile Ala Cys Pro Pro Leu	
130 135 140	

Gly Ala His Ile Arg Thr Leu Leu Leu Thr Phe Phe Tyr Arg Tyr Gln
115 120 125
Arg Ser Leu Leu Glu Gln Gly Tyr Met Tyr Ile Ala Cys Pro Pro Leu
130 135 140
Tyr Lys Leu Glu Arg Gly Arg Asn His Tyr Tyr Cys Tyr Asn Glu Arg
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Glu Leu Gln Glu Arg Ile Ala Thr Phe Pro Glu Asn Ala Asn Tyr Thr
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Ile

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Ile Ile Thr Ser Tyr Ala Glu Ser Ser Gly Ile Leu Lys Lys Glu Lys
20 25 30
gtc agc ctg ggc ggc gaa gac agc cgc gag ggc ctg acc tgc gtg ctg 144
Val Ser Leu Gly Gly Glu Asp Ser Arg Glu Gly Leu Thr Cys Val Leu
35 40 45

195 200 205 660
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Asn Pro Asp Lys Val Arg Tyr His Lys Ile Val Leu
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20 25 30
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35 40 45
Ser Val Lys Val Pro Asp Pro Lys Phe Ser Ser Gln Thr Lys Asp Lys
50 55 60
Leu Val Ser Ser Glu Val Arg Pro Ala Val Glu Gly Leu Val Ser Glu
65 70 75 80
Gly Leu Ser Thr Trp Phe Glu Glu His Pro Asn Glu Ala Lys Ala Ile
85 90 95
Val Thr Lys Ile Ala Glu Ala Ala Ala Arg Glu Ala Ala Arg Lys
100 105 110
Ala Arg Glu Leu Thr Arg Arg Lys Ser Ala Leu Asp Ile Thr Ser Leu
115 120 125
Pro Gly Lys Leu Ala Asp Cys Ser Glu Arg Asp Pro Ala Lys Ser Glu
130 135 140

Ile Phe Ile Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Ala
 145 150 155 160
 Arg Asn Arg Asp Asn Gln Ala Val Leu Pro Leu Arg Gly Lys Ile Leu
 165 170 175
 Asn Val Glu Arg Ala Arg Phe Asp Lys Met Leu Ser Ser Asp Gln Ile
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 Gly Thr Leu Ile Thr Ala Leu Gly Ala Gly Ile Gly Arg Asp Asp Phe
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 Ser Cys Val Asn Ala Leu Ser Asn Asn Leu Lys Ala Thr Val Tyr Arg
 20 25 30
 gaa ggt aaa ata tgg gag caa gag tat gaa aga ggt aag gct tta tat 144
 Glu Gly Lys Ile Trp Glu Gln Glu Tyr Glu Arg Gly Lys Ala Leu Tyr

35	40	45	
ccg gta aaa agt att gga gaa aca gag gaa aca ggt act ata gtt act	192		
Pro Val Lys Ser Ile Gly Glu Thr Glu Glu Thr Gly Thr Ile Val Thr			
50	55	60	
ttt tac cca gat gat act ata ttt aca caa act aca gag tat aat tat	240		
Phe Tyr Pro Asp Asp Thr Ile Phe Thr Gln Thr Thr Glu Tyr Asn Tyr			
65	70	75	80
gaa acg ctt tct aac aga atg cga gag ttg gct tac ctt aat aag gga	288		
Glu Thr Leu Ser Asn Arg Met Arg Glu Leu Ala Tyr Leu Asn Lys Gly			
85	90	95	
gtt aca att agc att aca gat aag aga gtt aaa gat gaa aag gga gag	336		
Val Thr Ile Ser Ile Thr Asp Lys Arg Val Lys Asp Glu Lys Gly Glu			
100	105	110	
ttt tta tct gaa gtt ttt tac tct gaa gaa gga cta aaa gaa ttt att	384		
Phe Leu Ser Glu Val Phe Tyr Ser Glu Glu Gly Leu Lys Glu Phe Ile			
115	120	125	
aag ttt tta gac ggt aac aga gaa caa cta ata cgt gat gtt gtt tca	432		
Lys Phe Leu Asp Gly Asn Arg Glu Gln Leu Ile Arg Asp Val Val Ser			
130	135	140	
atg gaa ggt gaa aaa aac gga att cct gtt gag gtt gca atg glg tac	480		
Met Glu Gly Glu Lys Asn Gly Ile Pro Val Glu Val Ala Met Val Tyr			
145	150	155	160
aat aca tca tat tca gaa aat ctt cac tct tac gta aat aat att aat	528		
Asn Thr Ser Tyr Ser Glu Asn Leu His Ser Tyr Val Asn Asn Ile Asn			
165	170	175	
aca cat gaa ggt ggt aca cac ctt tca ggt ttt aga aga ggt tta aca	576		
Thr His Glu Gly Gly Thr His Leu Ser Gly Phe Arg Arg Gly Leu Thr			
180	185	190	
tca acc tta aaa aag tat gca gat gca tct gga atg tta gac aaa tta	624		

Ser Thr Leu Lys Lys Tyr Ala Asp Ala Ser Gly Met Leu Asp Lys Leu	
195	200
aag ttt gag att cag gga gat gat ttt aga gaa ggt tta acg gct att	672
Lys Phe Glu Ile Gln Gly Asp Asp Phe Arg Glu Gly Leu Thr Ala Ile	
210	220
gtg tct gtt aaa gtt gca gaa cct cag ttt gaa ggg caa aca aaa act	720
Val Ser Val Lys Val Ala Glu Pro Gln Phe Glu Gly Gln Thr Lys Thr	
225	230
aaa tta ggt aac aga gaa gtt tct tct gca gtg agc caa gct gta tca	768
Lys Leu Gly Asn Arg Glu Val Ser Ser Ala Val Ser Gln Ala Val Ser	
245	250
gaa atg ctt acc aac tat tta gaa gaa aac cca gat gat gct aag gta	816
Glu Met Leu Thr Asn Tyr Leu Glu Glu Asn Pro Asp Asp Ala Lys Val	
260	270
att gla caa aaa gtc att ttg gca gcg caa gca cgt cat gcg gct aca	864
Ile Val Gln Lys Val Ile Leu Ala Ala Gln Ala Arg His Ala Ala Thr	
275	285
aaa gcc cgt gaa atg gta cag cgt aaa acg gta atg agt ata ggt ggt	912
Lys Ala Arg Glu Met Val Gln Arg Lys Thr Val Met Ser Ile Gly Gly	
290	300
tta cca ggg aaa tta tca gac tgt tct gag caa gat gct aca aaa tgc	960
Leu Pro Gly Lys Leu Ser Asp Cys Ser Glu Gln Asp Ala Thr Lys Cys	
305	310
gaa gta ttc ctt gta gag gga gat tcg gcg ggt ggt act gct aaa caa	1008
Glu Val Phe Leu Val Glu Gly Asp Ser Ala Gly Gly Thr Ala Lys Gln	
325	330
ggt agg gac aga aac ttt cag gca ata tta ccg ctt cgt ggt aaa atc	1056
Gly Arg Asp Arg Asn Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile	
340	350

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Asp Lys Asp Ser Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val

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5

10

15

Ser Cys Val Asn Ala Leu Ser Asn Asn Leu Lys Ala Thr Val Tyr Arg

20

25

30

Glu Gly Lys Ile Trp Glu Gln Glu Tyr Glu Arg Gly Lys Ala Leu Tyr

35

40

45

Pro Val Lys Ser Ile Gly Glu Thr Glu Glu Thr Gly Thr Ile Val Thr

50

55

60

Phe Tyr Pro Asp Asp Thr Ile Phe Thr Gln Thr Thr Glu Tyr Asn Tyr

65

70

75

80

Glu Thr Leu Ser Asn Arg Met Arg Glu Leu Ala Tyr Leu Asn Lys Gly

85

90

95

Val Thr Ile Ser Ile Thr Asp Lys Arg Val Lys Asp Glu Lys Gly Glu

100

105

110

Phe Leu Ser Glu Val Phe Tyr Ser Glu Glu Gly Leu Lys Glu Phe Ile

115

120

125

Lys Phe Leu Asp Gly Asn Arg Glu Gln Leu Ile Arg Asp Val Val Ser

130

135

140

Met Glu Gly Glu Lys Asn Gly Ile Pro Val Glu Val Ala Met Val Tyr

145

150

155

160

Asn Thr Ser Tyr Ser Glu Asn Leu His Ser Tyr Val Asn Asn Ile Asn

165

170

175

Thr His Glu Gly Gly Thr His Leu Ser Gly Phe Arg Arg Gly Leu Thr

180

185

190

Ser Thr Leu Lys Lys Tyr Ala Asp Ala Ser Gly Met Leu Asp Lys Leu

195

200

205

Lys Phe Glu Ile Gln Gly Asp Asp Phe Arg Glu Gly Leu Thr Ala Ile

Lys Arg Tyr Ala Trp Asn Asp Lys Glu Arg Asp Glu Ile Ala Glu Ser

450

455

460

Phe Asn Gly Ser Val Gly Ile Gln Arg Tyr

465

470

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tgtaaaacga cggccagtca ygcnggnggn aarttyga

<210> 26

<211> 7

<212> DNA

<213> Artificial Sequence

<400> 26

His Ala Gly Gly Lys Phe Asp

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<210> 27

<211> 36

<212> DNA

<213> Artificial Sequence

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ctgcgttcgt atatgagcnc crtcnacrte ngcrte

36

<210> 28

<211> 12

<212> PRT

<213> Artificial Sequence

<400> 28

Asp Ala Asp Val Asp Gly Ala His Ile Arg Thr Leu

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<210> 29

<211> 41

<212> DNA

<213> Artificial Sequence

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gaagtcacatca tgaccgttct gcaygsnggn ggnaarttyg g

41

<210> 30

<211> 14

<212> PRT

<213> Artificial Sequence

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Glu Val Leu Met Thr Val Leu His Ala Gly Gly Lys Phe Gly

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<210> 31

Sequence 6222860

<211> 44

<212> DNA

<213> Artificial Sequence

<400> 31

agcagggtac ggatgtgcga gccrtnacr tngcrtcng tgat 44

<210> 32

<211> 15

<212> PRT

<213> Artificial Sequence

<400> 32

Met Thr Asp Ala Asp Val Asp Gly Ser His Ile Arg Thr Leu Leu

1 5 10 15

<210> 33

<211> 32

<212> DNA

<213> Artificial Sequence

<400> 33

caggaaacag ctatgaccar rtgngtnccn cc 32

<210> 34

<211> 5

<212> PRT

<213> Artificial Sequence

<400> 34

Gly Gly Thr His Leu

1 5

<210> 35

<211> 34

<212> DNA

<213> Artificial Sequence

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gcaacgagat caacactcmn gargnggna cnca

34

<210> 36

<211> 11

<212> PRT

<213> Artificial Sequence

<400> 36

Asn Asn Ile Asn Thr His Glu Gly Gly Thr His

1 5 10

<210> 37

<211> 11

<212> PRT

<213> Artificial Sequence

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Asn Asn Ile Asn Thr Pro Glu Gly Gly Thr His

1 5 10

<210> 38

<211> 35

<212> DNA

<213> Artificial Sequence

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tgtaaaacga cggccagtar yttknkyyttt gtytg

35

<210> 39

<211> 6

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<213> Artificial Sequence

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Gln Thr Lys Thr Lys Leu

1 5

<210> 40

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<212> PRT

<213> Artificial Sequence

<400> 40

Gln Thr Lys Asp Lys Leu

1 5

<210> 41

<211> 35

<212> DNA

<213> Artificial Sequence

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taggctagct gaccgtaaga ygcngayrtn gaygg

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<210> 42

<211> 6

<212> PRT

<213> Artificial Sequence

<400> 42

Asp Ala Asp Val Asp Gly

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<210> 43

<211> 36

<212> DNA

<213> Artificial Sequence

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ccatagctgc gtagcattca tytncncnar nccytt

36

<210> 44

<211> 12

<212> PRT

<213> Artificial Sequence

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Lys Gly Leu Gly Glu Met Asn Ala Thr Gln Leu Trp

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<210> 45

<211> 41

<212> DNA

<213> Artificial Sequence

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<212> PRT

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<400> 46

Lys Arg Pro Ala Met Tyr Ile Gly

1 5

<210> 47

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<212> PRT

<213> Artificial Sequence

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Lys Arg Pro Gly Met Tyr Ile Gly

1 5

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Gln Leu Trp Glu Thr Thr Met

1 5

<210> 52

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<212> PRT

<213> Artificial Sequence

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Gln Leu Trp Asp Thr Thr Met

1 5

<210> 53

<211> 41

<212> DNA

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<210> 54

<211> 14

<212> PRT

<213> Artificial Sequence

<400> 54

Glu Val Ile Met Thr Val Leu His Ala Gly Gly Lys Phe Asp

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Thr Asn Asn Ile Pro Gln

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<210> 62

<211> 38

<212> DNA

<213> Artificial Sequence

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tgtaaaacga cggccagtaa yttnggntcn ggnacytt 38

<210> 63

<211> 7

<212> PRT

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Lys Val Pro Asp Pro Lys Phe

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<212> PRT

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Lys Val Pro Glu Pro Lys Phe

1

5

<210> 65

<211> 35

<212> DNA

<213> Artificial Sequence

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caggaaacag ctatgaccgc nmrnmrngcn mgnga

35

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<211> 6

<212> PRT

<213> Artificial Sequence

<400> 66

Ala Arg Arg Ala Arg Glu

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Ala Arg Lys Ala Arg Glu

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Ala Lys Lys Ala Arg Glu

1 5

<210> 69

<211> 19

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Pro or Ser; Xaa2 = Ala or Thr; Xaa3 = Ala, Val or Leu; Xaa4 = Glu or Asp;
Xaa5 = Val or Thr; Xaa6 = Ile or Val; Xaa7 = Met, Leu or Phe; Xaa8 = Val, Gln or Ile;
Xaa9 = Asp or Gly; Xaa10 = Asp, Gly, Asn or Ser; Xaa11 = Ser, Lys, Gly, Asp or Asn

<400> 69

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Xaa Leu His Ala Gly Gly Lys Phe

1 5 10 15

Xaa Xaa Xaa

<210> 70

<211> 4

<212> PRT

<213> Artificial Sequence

<400> 70

Gly Gly Thr His

1

<210> 71

<211> 15

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Ile or Leu; Xaa2 = Ala or Ser

<400> 71

Xaa Met Thr Asp Ala Asp Val Asp Gly Xaa His Ile Arg Thr Leu

1 5 10 15

<210> 72

<211> 11

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Gly or Ala; Xaa2 = Ser or Asp

<400> 72

Arg Lys Arg Pro Xaa Met Tyr Ile Gly Xaa Thr

1 5 10

<210> 73

<211> 6

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Thr or Pro; Xaa2 = Lys or Asn; Xaa3 = Thr, Asp, Gly, Lys, Ser, Phe or Tyr

<400> 73

Gln Xaa Xaa Xaa Lys Leu

1 5

<210> 74

<211> 9

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Tyr or Phe; Xaa2 = Ala or Pro

<400> 74

Xaa Lys Gly Leu Gly Glu Met Asn Xaa

1 5

<210> 75

<211> 9

<212> PRT

<213> Artificial Sequence

<400> 75

Val Glu Gly Asp Ser Ala Gly Gly Ser

1 5

<210> 76

<211> 7

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = His or Val; Xaa2 = Gln or Lys

<400> 76

Lys Xaa Pro Asp Pro Xaa Phe

1 5

<210> 77

<211> 14

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Ser or Gln; Xaa2 = Ser or Glu; Xaa3 = Lys or Arg; Xaa4 = Ala or Ser

<400> 77

Leu Pro Gly Lys Leu Ala Asp Cys Xaa Xaa Xaa Asp Pro Xaa

1 5 10

<210> 78

<211> 9

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Trp or Arg; Xaa2 = Glu or Asp; Xaa3 = Met or Leu; Xaa4 = Asp or Asn

<400> 78

Gln Leu Xaa Xaa Thr Thr Xaa Xaa Pro

1 5

<210> 79

<211> 6

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Lys or Arg; Xaa2 = Lys or Arg

<400> 79

Ala Xaa Xaa Ala Arg Glu

1 5

<210> 80

<211> 7

<212> PRT

<213> Artificial Sequence

<223> Xaa1 = Pro or Asn; Xaa2 = Thr or Gln

<400> 80

Phe Thr Asn Asn Ile Xaa Xaa

1

5

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